

## RAW SEQUENCE LISTING

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Information Center (STIC) no errors detected.**

Application Serial Number: 10/528,748  
Source: PCT  
Date Processed by STIC: 3-30-05

# ***ENTERED***



PCT

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DATE: 03/30/2005

PATENT APPLICATION: US/10/528,748

TIME: 14:14:12

Input Set : A:\NHL-NP-49-NP.ST25.txt

Output Set: N:\CRF4\03302005\J528748.raw

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3 <110> APPLICANT: JUNGHANS, Claas
4     SCHROFF, Matthias
5     JUHLS, Christiane
6     OSWALD, Detlef
8 <120> TITLE OF INVENTION: Vaccine against Oncovirus Infections, such as infections by
9     Feline leukosis virus of the cat
11 <130> FILE REFERENCE: NHL-NP-49-NP
C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/528,748
C--> 13 <141> CURRENT FILING DATE: 2005-03-22
13 <150> PRIOR APPLICATION NUMBER: DE 102 44 863.9
14 <151> PRIOR FILING DATE: 2002-09-23
16 <150> PRIOR APPLICATION NUMBER: PCT/DE2003/003179
17 <151> PRIOR FILING DATE: 2003-09-19
19 <160> NUMBER OF SEQ ID NOS: 40
21 <170> SOFTWARE: PatentIn version 3.3
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 1929
25 <212> TYPE: DNA
26 <213> ORGANISM: Feline leukemia virus
29 <220> FEATURE:
30 <221> NAME/KEY: gene
31 <222> LOCATION: (1)..(1929)
32 <223> OTHER INFORMATION: DNA sequence wild type "env" gene without signal peptide
coding
33     region
35 <300> PUBLICATION INFORMATION:
36 <308> DATABASE ACCESSION NO: NCBI M12500
37 <309> DATABASE ENTRY DATE: 2001-02-21
38 <313> RELEVANT RESIDUES: (162)..(1990)
40 <400> SEQUENCE: 1
41 atggaaagtc caacgcaccc aaaaccctct aaagataaga ctctctcgtg gaacttagcg      60
43 tttctggtgg g gatcttatt tacaatagac ataggaatgg ccaatcctag tccacaccaa      120
45 atatataatg taacttgggt aataaccaat gtacaaacta acaccaagc taacgccacc      180
47 tctatgttag gaaccttaac cgatgcctac cctaccctac atgttgactt atgtgacctt      240
49 gtgggagaca cctgggaacc tatagtccta aaccaacca atgtaaaaca cggggcacgt      300
51 tactcctcct caaaatatgg atgtaaaact acagatagaa aaaaacagca acagacatac      360
53 cccttttacg tctgccccgg acatgcccc cgttgggggc caaagggaac acattgtgga      420
55 ggggcacaag atgggttttg tgccgcatgg g gatgtgaga ccaccggaga agcttggtgg      480
57 aagccacact cctcatggga ctatatcaca gtaaaaagag ggagtagtca ggacaatagc      540
59 tgtgagggaa aatgcaaccc cctggttttg cagttcaccc agaagggaag acaagcctct      600
61 tgggacggac ctaagatgtg gggattgcga ctataccgta caggatatga ccctatcgct      660
63 ttattcacgg tgtcccggca ggtatcaacc attacgccgc ctcaggcaat gggaccaaac      720
65 ctagtcttac ctgatcaaaa acccccatcc cgacaatctc aaacagggtc caaagtggcg      780
67 acccagaggc cccaaacgaa tgaaagcgcc ccaaggtctg ttgccccac caccatgggt      840

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69 cccaaacgga ttgggaccgg agatagggtta ataaatttag tacaagggac atacctagcc 900
71 ttaaatgccca ccgaccccaa caaaactaaa gactgttggc tctgcctggg ttctcgacca 960
73 ccctattacg aagggattgc aatcttaggt aactacagca accaaacaaa ccccccccca 1020
75 tcctgcctat ctactccgca acacaaacta actatatctg aagtatcagg gcaagggaatg 1080
77 tgcataggga ctgttcctaa aacccaccag gctttgtgca ataagacaca acagggacat 1140
79 acagggggcg actatctagc cgcccccaac ggcacctatt gggcctgtaa cactggactc 1200
81 accccatgca tttccatggc ggtgctcaat tggacctctg atttttgtgt cttaatcgaa 1260
83 ttatggccca gagtgcacta ccatcaaccc gaatatgtgt acacacattt tgccaaagct 1320
85 gtcagggtcc gaagagaacc aatatcacta acggttgccc ttatgttggg aggacttact 1380
87 gttagggggc tagccgcggg ggtcgggaaca gggactaaag ccctccttga aacagcccag 1440
89 ttcagacaac tacaaatggc catgcacaca gacatccagg ccctagaaga atcaattagt 1500
91 gccttagaaa agtccctgac ctccccttct gaagtagtct taaaaaacag acggggccta 1560
93 gatattctat tcttacaaga gggagggctc tgtgccgcat tgaaagaaga atgttgcttc 1620
95 tatgcggatc acaccggact cgtccgagac aatatggcca aattaagaga aagactaaaa 1680
97 cagcggcaac aactgtttga ctcccaacag ggatggtttg aaggatggtt caacaagtcc 1740
99 ccctggttta caaccctaatt ttcctccatt atgggcccct tactaatcct actcctaatt 1800
101 ctctctctcg gccatgcat ccttaaccga ttagtacaat tcgtaaaaga cagaatatct 1860
103 gtggtacagg cttaattttt aaccaacag taccaacaga taaagcaata cgatccggac 1920
105 cgaccatga 1929
108 <210> SEQ ID NO: 2
109 <211> LENGTH: 1527
110 <212> TYPE: DNA
111 <213> ORGANISM: Feline leukemia virus
114 <220> FEATURE:
115 <221> NAME/KEY: gene
116 <222> LOCATION: (1)..(1527)
117 <223> OTHER INFORMATION: DNA sequence wild type "gag" gene
119 <400> SEQUENCE: 2
120 atgggccaaa ctataactac ccccttgagc ctcaccctca accactggtc tgaggttcag 60
122 gcacggggccc gtaatcaggg tgtcgaagtc cggaaaaaga aatggattac actgtgtgaa 120
124 gccgaatggg taatgatgaa ttagaggttg ccccgagaag gaactttcac cattgacaat 180
126 atttcacagg tcgaggagag aatcttcgcc ccggggccat atggacaccc agatcaaadc 240
128 ctttatatta ccacgtggag atccctagcc acagaccccc ctccatgggt tcgccattc 300
130 ctaccccctc ctaagcatcc caggacagat cctcccagac ctctttcgcc gcaacctctt 360
132 gcgcccgaac cctcttcccc ccaccccgtc ctctaccccg ttctcccaa accagacccc 420
134 cccaaggcgc ctgtattacc acccaatcct tcttcccctt taattgatct cttaacagaa 480
136 gagccacctc cctatcctgg gggtcacggg ccaacaccgc cgtcaggccc tagaacccca 540
138 actgctctcc cgattgccat ccggctgcga gaacgacgag aaaatccagc tgagaaatct 600
140 caagccctcc ccttaaggga agacccaaac aacagacccc agtactggcc attctcggcc 660
142 tctgacctgt acaattggaa attgcataac ccccttttct ccaggacccc agtggcccta 720
144 actaacctaa ttgagtccat tttagtgaac catcagccaa cctgggacga ctgccaacag 780
146 ctcttacagg ctctcctgac ggcagaggag agacaaaggg tcctccttga agcccgaag 840
148 caagttccag gcgaggacgg acggccaacc cagctgccca atgtcgttga cgaggctttc 900
150 cccttgaccc gtcccaactg ggatttttgt acgcggcgag gtaggagca cctacgcctt 960
152 tatcgccagt tgctgttagc ggggctccgc ggggctgcaa gacgcccac taatttggca 1020
154 caggtaaagc aagttgtaca agggaaagag gaaacgccag cctcattctt agaaagatta 1080
156 aaagaggctt acagaatgta tactccctat gacctgagg acccagggca ggctgctagt 1140
158 gttatcctgt ctttatcta ccagtctagc ccggacataa gaaataagtt acaagggcta 1200
160 gaaggcctac aggggttcac actgtctgat ttgctaaaaa aggcagaaaa gatatacaac 1260

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162 aaaagggaaa ccccagagga aaggaagaa agattatggc agcggcagga agaaagagat 1320
164 aaaaagcgcc ataaggagat gactaaagt ctggccacag tagttgctca gaatagagat 1380
166 aaggatagag gggaaagtaa actgggagat caaaggaaaa tacctctggg gaaagaccag 1440
168 tgtgcctatt gcaaggaaaa gggacattgg gttcgcgatt gcccgaacg accccggaag 1500
170 aaacccgcca actccactct cctctaa 1527
173 <210> SEQ ID NO: 3
174 <211> LENGTH: 642
175 <212> TYPE: PRT
176 <213> ORGANISM: Feline leukemia virus
179 <220> FEATURE:
180 <221> NAME/KEY: PEPTIDE
181 <222> LOCATION: (1)..(447)
182 <223> OTHER INFORMATION: Amino acid sequence of the protein corresponding to Seq.ID1
184 <400> SEQUENCE: 3
186 Met Glu Ser Pro Thr His Pro Lys Pro Ser Lys Asp Lys Thr Leu Ser
187 1 5 10 15
190 Trp Asn Leu Ala Phe Leu Val Gly Ile Leu Phe Thr Ile Asp Ile Gly
191 20 25 30
194 Met Ala Asn Pro Ser Pro His Gln Ile Tyr Asn Val Thr Trp Val Ile
195 35 40 45
198 Thr Asn Val Gln Thr Asn Thr Gln Ala Asn Ala Thr Ser Met Leu Gly
199 50 55 60
202 Thr Leu Thr Asp Ala Tyr Pro Thr Leu His Val Asp Leu Cys Asp Leu
203 65 70 75 80
206 Val Gly Asp Thr Trp Glu Pro Ile Val Leu Asn Pro Thr Asn Val Lys
207 85 90 95
210 His Gly Ala Arg Tyr Ser Ser Ser Lys Tyr Gly Cys Lys Thr Thr Asp
211 100 105 110
214 Arg Lys Lys Gln Gln Gln Thr Tyr Pro Phe Tyr Val Cys Pro Gly His
215 115 120 125
218 Ala Pro Ser Leu Gly Pro Lys Gly Thr His Cys Gly Gly Ala Gln Asp
219 130 135 140
222 Gly Phe Cys Ala Ala Trp Gly Cys Glu Thr Thr Gly Glu Ala Trp Trp
223 145 150 155 160
226 Lys Pro Thr Ser Ser Trp Asp Tyr Ile Thr Val Lys Arg Gly Ser Ser
227 165 170 175
230 Gln Asp Asn Ser Cys Glu Gly Lys Cys Asn Pro Leu Val Leu Gln Phe
231 180 185 190
234 Thr Gln Lys Gly Arg Gln Ala Ser Trp Asp Gly Pro Lys Met Trp Gly
235 195 200 205
238 Leu Arg Leu Tyr Arg Thr Gly Tyr Asp Pro Ile Ala Leu Phe Thr Val
239 210 215 220
242 Ser Arg Gln Val Ser Thr Ile Thr Pro Pro Gln Ala Met Gly Pro Asn
243 225 230 235 240
246 Leu Val Leu Pro Asp Gln Lys Pro Pro Ser Arg Gln Ser Gln Thr Gly
247 245 250 255
250 Ser Lys Val Ala Thr Gln Arg Pro Gln Thr Asn Glu Ser Ala Pro Arg
251 260 265 270
254 Ser Val Ala Pro Thr Thr Met Gly Pro Lys Arg Ile Gly Thr Gly Asp

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255          275          280          285
258 Arg Leu Ile Asn Leu Val Gln Gly Thr Tyr Leu Ala Leu Asn Ala Thr
259          290          295          300
262 Asp Pro Asn Lys Thr Lys Asp Cys Trp Leu Cys Leu Val Ser Arg Pro
263 305          310          315          320
266 Pro Tyr Tyr Glu Gly Ile Ala Ile Leu Gly Asn Tyr Ser Asn Gln Thr
267          325          330          335
270 Asn Pro Pro Pro Ser Cys Leu Ser Thr Pro Gln His Lys Leu Thr Ile
271          340          345          350
274 Ser Glu Val Ser Gly Gln Gly Met Cys Ile Gly Thr Val Pro Lys Thr
275          355          360          365
278 His Gln Ala Leu Cys Asn Lys Thr Gln Gln Gly His Thr Gly Ala His
279          370          375          380
282 Tyr Leu Ala Ala Pro Asn Gly Thr Tyr Trp Ala Cys Asn Thr Gly Leu
283 385          390          395          400
286 Thr Pro Cys Ile Ser Met Ala Val Leu Asn Trp Thr Ser Asp Phe Cys
287          405          410          415
290 Val Leu Ile Glu Leu Trp Pro Arg Val Thr Tyr His Gln Pro Glu Tyr
291          420          425          430
294 Val Tyr Thr His Phe Ala Lys Ala Val Arg Phe Arg Arg Glu Pro Ile
295          435          440          445
298 Ser Leu Thr Val Ala Leu Met Leu Gly Gly Leu Thr Val Gly Gly Ile
299          450          455          460
302 Ala Ala Gly Val Gly Thr Gly Thr Lys Ala Leu Leu Glu Thr Ala Gln
303 465          470          475          480
306 Phe Arg Gln Leu Gln Met Ala Met His Thr Asp Ile Gln Ala Leu Glu
307          485          490          495
310 Glu Ser Ile Ser Ala Leu Glu Lys Ser Leu Thr Ser Leu Ser Glu Val
311          500          505          510
314 Val Leu Gln Asn Arg Arg Gly Leu Asp Ile Leu Phe Leu Gln Glu Gly
315          515          520          525
318 Gly Leu Cys Ala Ala Leu Lys Glu Glu Cys Cys Phe Tyr Ala Asp His
319          530          535          540
322 Thr Gly Leu Val Arg Asp Asn Met Ala Lys Leu Arg Glu Arg Leu Lys
323 545          550          555          560
326 Gln Arg Gln Gln Leu Phe Asp Ser Gln Gln Gly Trp Phe Glu Gly Trp
327          565          570          575
330 Phe Asn Lys Ser Pro Trp Phe Thr Thr Leu Ile Ser Ser Ile Met Gly
331          580          585          590
334 Pro Leu Leu Ile Leu Leu Leu Ile Leu Leu Phe Gly Pro Cys Ile Leu
335          595          600          605
338 Asn Arg Leu Val Gln Phe Val Lys Asp Arg Ile Ser Val Val Gln Ala
339          610          615          620
342 Leu Ile Leu Thr Gln Gln Tyr Gln Gln Ile Lys Gln Tyr Asp Pro Asp
343 625          630          635          640
346 Arg Pro
350 <210> SEQ ID NO: 4
351 <211> LENGTH: 508
352 <212> TYPE: PRT

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353 <213> ORGANISM: Feline leukemia virus
356 <220> FEATURE:
357 <221> NAME/KEY: PEPTIDE
358 <222> LOCATION: (1)..(508)
359 <223> OTHER INFORMATION: Amino acid sequence of the protein corresponding to Seq.ID2
361 <400> SEQUENCE: 4
363 Met Gly Gln Thr Ile Thr Thr Pro Leu Ser Leu Thr Leu Asn His Trp
364 1 5 10 15
367 Ser Glu Val Gln Ala Arg Ala Arg Asn Gln Gly Val Glu Val Arg Lys
368 20 25 30
371 Lys Lys Trp Ile Thr Leu Cys Glu Ala Glu Trp Val Met Met Asn Val
372 35 40 45
375 Gly Trp Pro Arg Glu Gly Thr Phe Thr Ile Asp Asn Ile Ser Gln Val
376 50 55 60
379 Glu Glu Arg Ile Phe Ala Pro Gly Pro Tyr Gly His Pro Asp Gln Ile
380 65 70 75 80
383 Pro Tyr Ile Thr Thr Trp Arg Ser Leu Ala Thr Asp Pro Pro Pro Trp
384 85 90 95
387 Val Arg Pro Phe Leu Pro Pro Pro Lys His Pro Arg Thr Asp Pro Pro
388 100 105 110
391 Glu Pro Leu Ser Pro Gln Pro Leu Ala Pro Gln Pro Ser Ser Pro His
392 115 120 125
395 Pro Val Leu Tyr Pro Val Leu Pro Lys Pro Asp Pro Pro Lys Ala Pro
396 130 135 140
399 Val Leu Pro Pro Asn Pro Ser Ser Pro Leu Ile Asp Leu Leu Thr Glu
400 145 150 155 160
403 Glu Pro Pro Pro Tyr Pro Gly Gly His Gly Pro Thr Pro Pro Ser Gly
404 165 170 175
407 Pro Arg Thr Pro Thr Ala Ser Pro Ile Ala Ile Arg Leu Arg Glu Arg
408 180 185 190
411 Arg Glu Asn Pro Ala Glu Lys Ser Gln Ala Leu Pro Leu Arg Glu Asp
412 195 200 205
415 Pro Asn Asn Arg Pro Gln Tyr Trp Pro Phe Ser Ala Ser Asp Leu Tyr
416 210 215 220
419 Asn Trp Lys Leu His Asn Pro Pro Phe Ser Gln Asp Pro Val Ala Leu
420 225 230 235 240
423 Thr Asn Leu Ile Glu Ser Ile Leu Val Thr His Gln Pro Thr Trp Asp
424 245 250 255
427 Asp Cys Gln Gln Leu Leu Gln Ala Leu Leu Thr Ala Glu Glu Arg Gln
428 260 265 270
431 Arg Val Leu Leu Glu Ala Arg Lys Gln Val Pro Gly Glu Asp Gly Arg
432 275 280 285
435 Pro Thr Gln Leu Pro Asn Val Val Asp Glu Ala Phe Pro Leu Thr Arg
436 290 295 300
439 Pro Asn Trp Asp Phe Cys Thr Pro Ala Gly Arg Glu His Leu Arg Leu
440 305 310 315 320
443 Tyr Arg Gln Leu Leu Leu Ala Gly Leu Arg Gly Ala Ala Arg Arg Pro
444 325 330 335
447 Thr Asn Leu Ala Gln Val Lys Gln Val Val Gln Gly Lys Glu Glu Thr

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**VERIFICATION SUMMARY**

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Input Set : A:\NHL-NP-49-NP.ST25.txt

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L:13 M:270 C: Current Application Number differs, Replaced Current Application No

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date